

1	GAATTGGCC	CTGAGGCCA	AGAAATTCGG	ACGAGGCGG	CGCGGTCGC	TGCTCCGCG	TGCTCCGCG	CGCGGTCGC	GTCCGTCGC	CGACAGCGT	GGCCCCGCG	GCTGTCCG	CACCCGCAT	GGGGCTCTCC
1	CTTAAACCG	GAGCTCCGGT	TCTTAAGCCG	TGCTCCGCG	TGCTCCGCG	TGCTCCGCG	TGCTCCGCG	TGCTCCGCG	TGCTCCGCG	TGCTCCGCG	TGCTCCGCG	TGCTCCGCG	TGCTCCGCG	TGCTCCGCG
101	TGGAGCCCG	GACCTCCACT	GCTGATGATC	CTGCTACTGG	TGCTGTCTGT	GTGGCTGCCA	CTTGGAGCAG	GAAACTCCCT	TGCCACAGAG	AACAGGTTTG	TTGTCCAAAC	TTGTCCAAAC	TTGTCCAAAC	TTGTCCAAAC
5	TrpSerProA	rgProProLe	uLeuMetIle	LeuLeuLeuV	alleuSerLe	uTrpLeuPro	LeuGlyAlaG	lyAsnSerLe	uAlaThrGlu	AsnArgPheVal				
201	TGAACAGCTG	TACCCAGGCC	AGAAAGAAAT	CGCAGGCTAA	TCCCGCTTGC	AAGGCTGCCT	ACCAGCACCT	GGGCTCCTGC	ACCTCCAGTT	TAAGCAGGCC				
39	AsnSerCy	sThrGlnAla	ArgLysLysC	ysGluAlaAs	nProAlaCys	LysAlaAlaT	yrGlnHisLe	uGlySerCys	ThrSerSerL	euSerArgPro				
301	GCTGCCCTTA	GAGGAGTCTG	CCATGTCTGC	AGACTGCCTA	GAGGAGCAG	AACAACCTCAG	GAACAGCTCT	CTGATAGACT	GCAGGTGCCA	TCGGCGCATG				
72	LeuProLeu	GluGluSerA	laMetSerAl	aAspCysLeu	GluAlaAlaG	luGlnLeuAr	gAsnSerSer	LeulleAspC	ysArgCysHi	sArgArgMet				
401	AAGCACCAAG	CTACTGTCTT	GGACATTTAT	TGGACCGTTC	ACCCTGCCCG	AAGCCTTGGT	GACTACGAGT	TGGATGTCTC	ACCCATATGA	GACACAGTGA				
105	LysHisGlnA	laThrCysLe	uAspIleTyr	TrpThrValH	isProAlaAr	gSerLeuGly	AspTyrGluL	euAspValSe	rProTyrGlu	AspThrValThr				
501	CCAGCAAAAC	CTGGAATAATG	AATCTTAGCA	AGTTGAACAT	GCTCAAACCA	GACTCGGACC	TCTGCCTCAA	ATTTGCTATG	CTGTGTACTC	TTACACGACAA				
139	SerLysPr	oTrpLysMet	AsnLeuSerL	ysLeuAsnMe	tLeuLysPro	AspSerAspL	euCysLeuLy	sPheAlaMet	LeuCysThrL	euHisAspLys				
601	CTGTGACCGC	CTGCGCAAGG	CCTACGGGGA	GGCATCGCTCA	GGGATCCGCT	GCCAGCGCCA	CCTCTGCCTA	GCCAGCTGCG	GCTCCTTCTT	TGAGAAGGCA				
172	CysAspArg	LeuArgLysA	laTyrGlyGL	uAlaCysSer	GlyIleArgC	ysGlnArgHi	sLeuCysLeu	AlaGlnLeuA	rgSerPhePh	eGluLysAla				
701	GCAGAGTCCC	ACGCTCAGGG	TCTGTCTGCTG	TGTCCCTGTG	CACCAAGAAG	TGCGGGCTGT	GGGAGCGCG	GGCGTAACAC	CATCGCCCCC	AGTTGCGCCC				
205	AlaGluSerH	isAlaGlnGL	yLeuLeuLeu	CysProCysA	laProGluAs	pAlaGlyCys	GlyGluArgA	rgArgAsnTh	rIleAlaPro	SerCysAlaLeu				
801	TGCCTTCTGT	AACCCCAAT	TGCCTGGATC	TGCGGAGCTT	CTGCCCTGCG	GACCCCTTGT	GCAGATCACC	CCTGATGGAC	TTCCAGACCC	ACTGTTCATCC				
239	ProSerVa	lThrProAsn	CysLeuAspL	euArgSerPh	eCysArgAla	AspProLeuC	ysArgSerAr	gLeuMetAsp	PheGlnThrH	isCysHisPro				
901	TATGACATC	CTTTGGACTT	GTGCAACTGA	GCAATCCAGA	TGCTCTGCGG	CATACCTGGG	GCTGATTTGG	ACTGCCATGA	CCCCAACTT	CATCAGCAAG				
272	MetaSpille	LeuGlyThrC	ysAlaThrGL	uGlnSerArg	CysLeuArgA	laTyrLeuGL	yLeuIleGly	ThrAlaMetT	hrProAsnPh	eIleSerLys				

FIG. 1A

1001 GTCAACACTA CTGTTGCCCTT AAGCTGCACC TGCCGAGGCA GCGCAACCT ACAGGACGAG TGTGAACAGC TGGAAAGGTC CTTCTCCCAG AACCCCTGCC
CAGTTGTGAT GACAACGGAA TTCCAGCGTG ACGGCTCGGT CGCCGTTGGA TGTCTGCTC ACATTGTCTG ACCTTTCCAG GAAGAGGTC TTGGGGACGG
305 ValAsnThrT hrValAlaLe uSerCysThr CysArgGlys erGlyAsnLe uGlnAspGlu CysGluGlnL euGluArgSe rPheSerGln AsnProCysLeu
1101 TCGTGGAGGC CATTGCAGCT AAGATGCGTT TCCACAGACA GCTCTTCTCC CAGGACTGGG CAGACTCTAC TTTTTCAGTG GTGCAGCAGC AGAACAGCAA
AGCACCTCG GTAACGTCGA TTCTACGCAA AGGTGTCTGT CGAGAAGAGG GTCTGACCC GTCTGAGATG AAAAAGTCAC CACGTCGTCG TCTTGTCTGT
339 ValGluAl aileAlaAla LysMetArgp heHisArgGl nLeuPheSer GlnAspTrpA laAspSerTh rPheSerVal ValGlnGlnG InAsnSerAsn
1201 CCCTGCTCTG AGACTGCAGC CCAGGCTACC CATTCTTTCT TTCTCCATCC TTCTCTGAT TCTGTGCAG ACCCTCTGGT AGCTGGGCTT CCTCAGGGTC
GGGACGAGAC TCTGACGTCG GGTCGATGG GTAAGAAAGA AAGAGGTAGG AAGGAACTA AGACGAGTC TGGGAGACCA TCGACCCGAA GGAGTCCCAG
372 ProAlaLeu ArgLeuGlnP roArgLeuPr oileLeuSer PheSerIleL euProLeuIl eLeuLeuGln ThrLeuTrp
1301 CTTTGTCTC TCCACCACAC CCAGACTGAT TTGCAGCCTG TGGTGGGAGA GAACTCGCCA GCCTGTGGAA CGTGTACAC AGCAACCCCG
GAAACAGGAG AGGTGGTGTG GGTCTGACTA AACGTCGGAC ACCACCTCT CTTGAGCGGT CGGACACCTT CTCTGCGTC GCAGATGTG TCGTTGGGCC
1401 AACCAACCAG GCATTCCGCA GCACATCCCG TCTGCTCCAG AAGAGGTCTT AGAAGTGAGG GCTGTGACCC TTCCGATCCT GAGCGCTAG TTTTCAAACC
TTGGTTGGTC CGTAAGCGT CGTGTAGGC AGACGAGTC TTCTCCAGAA TCTTCACTCC CGACACTGG AAGGCTAGGA CTCGCCGATC AAAAGTTTGG
1501 TCCCTTGCCC CTGCTTCCTT CTGGCTCAGG CTGCTCCTCC TTAGGACTTT GTGGTCCAG TTTTGCCTTC TGTCTGTATG GTGATTAGCG GCTCACCTCC
AGGGAACGGG GACGAAGGAA GACCGAGTCC GACGAGGAG AATCCTGAAA CACCAGGTC AAAACGGAA ACAAGACTAC CACTAATCGC CGAGTGGAGG
1601 AGCGCTTCTT CCTGTTTCCC AGGACCACCC AGAGGCTAAG GAATCAGTCA TTCCCTGTTG CCTTCTCCAG GAAGGCAGGC TAAGGCTTCT GAGGTGACTG
TCGCGAAGAA GGACAAAGG TCCTGGTGGG TCTCCGATT CTTAGTCAGT AAGGGACAAC GGAAGAGGTC CTTCCGTCG ATTCCCAAGA CTCCACTGAC
1701 AGAAAAATGT TTCTTTTGTG TGAAGGCTG GTGCTCCAGC CTCACGTCCT CTCTGAATGG AAGATAAAAA CCTGCTGGTG TCTTGACTGC TCTGCCAGGC
TCITTTTACA AAGGAAACAC ACCTTCCGAC CACGAGGTG CACGAGGTG GAGACTTACC TTCTATTTTTT GGACGACCAC AGAAGTACG AGACGGTCCG
1801 AATCCTGAAC ATTGGGCAT GAAGAGCTAA AGTCTTTGG TCTTGTTTAA CTCCTATTAC TGTCCCCAAA TTCCCCTAGT CCTTGGGTC ATGATTAAAC
TTAGGACTTG TAAACCCGTA CTTCTCGATT TCAGAAACCC AGAACAAATT GAGGATAATG ACAGGGTTT AAGGGGATCA GGGAAACCCAG TACTAATTTG
1901 ATTTTGACTT AAAAAAAA AAAA AAAA
TAAACTGAA TTTTTTTTTT TTTTTT

FIG. 1B

FIG. 2

FIG. 2

hGFra3	1	M	V	R	P	L	N	P	R	P	L	P	P	V	V	L	M	L	L	L	L	L	P	P	S	P	L	P	L	A	G	D	P	L	P	T	E	S	R	L	M	N	S	C	L	Q	A	R	R	K	
mGFra3	1	-	-	M	G	L	S	W	S	P	R	P	P	L	L	M	I	L	L	L	V	L	S	L	W	-	L	P	L	G	A	G	N	S	L	A	T	E	N	R	F	V	N	S	C	T	Q	A	R	K	K
hGFra3	51	C	Q	A	D	P	T	C	S	A	A	Y	H	L	D	S	C	T	S	S	I	S	T	P	L	S	E	E	P	S	V	P	A	D	C	L	E	A	A	Q	L	R	N	S	S	L	I	G			
mGFra3	48	C	E	A	N	P	A	C	K	A	A	Y	Q	H	L	G	S	C	T	S	S	L	S	R	P	L	P	L	E	E	S	A	M	S	A	D	C	L	E	A	A	E	Q	L	R	N	S	S	L	I	D
hGFra3	101	C	M	C	H	R	R	M	K	N	Q	V	A	C	L	D	I	Y	W	T	V	H	R	A	R	S	L	G	N	Y	E	L	D	V	S	P	Y	E	D	T	V	T	S	K	P	W	K	M	N	L	S
mGFra3	98	C	R	C	H	R	R	M	K	H	Q	A	T	C	L	D	I	Y	W	T	V	H	P	A	R	S	L	G	D	Y	E	L	D	V	S	P	Y	E	D	T	V	T	S	K	P	W	K	M	N	L	S
hGFra3	151	K	L	N	M	L	K	P	D	S	D	L	C	L	K	F	A	M	L	C	T	L	N	D	K	C	D	R	L	R	K	A	Y	G	E	A	C	S	G	P	H	C	Q	R	H	V	C	L	R	Q	L
mGFra3	148	K	L	N	M	L	K	P	D	S	D	L	C	L	K	F	A	M	L	C	T	L	H	D	K	C	D	R	L	R	K	A	Y	G	E	A	C	S	G	I	R	C	Q	R	H	L	C	L	A	Q	L
hGFra3	201	L	T	F	F	E	K	A	A	E	P	H	A	Q	G	L	L	L	C	P	C	A	P	N	D	R	G	C	G	E	R	R	R	N	T	I	A	P	N	C	A	L	P	P	V	A	P	N	C	L	E
mGFra3	198	R	S	F	F	E	K	A	A	E	S	H	A	Q	G	L	L	L	C	P	C	A	P	E	D	A	G	C	G	E	R	R	R	N	T	I	A	P	S	C	A	L	P	S	V	T	P	N	C	L	D
hGFra3	251	L	R	L	C	F	S	D	P	L	C	R	S	R	L	V	D	F	Q	T	H	C	H	P	M	D	I	L	G	T	C	A	T	E	Q	S	R	C	L	R	A	Y	L	G	L	I	G	T	A	M	
mGFra3	248	L	R	S	F	C	R	A	D	P	L	C	R	S	R	L	M	D	F	Q	T	H	C	H	P	M	D	I	L	G	T	C	A	T	E	Q	S	R	C	L	R	A	Y	L	G	L	I	G	T	A	M
hGFra3	301	T	P	N	F	V	S	N	V	N	T	S	V	A	L	S	C	T	C	R	G	S	G	N	L	Q	E	E	C	E	M	L	E	G	F	F	S	H	N	P	C	L	T	E	A	I	A	A	K	M	R
mGFra3	298	T	P	N	F	I	S	K	V	N	T	I	S	V	A	L	S	C	T	C	R	G	S	G	N	L	Q	E	C	E	Q	L	E	R	S	F	S	Q	N	P	C	L	V	E	A	I	A	A	K	M	R
hGFra3	351	F	H	S	Q	L	F	S	Q	D	W	P	H	P	T	F	A	V	M	A	H	Q	N	E	N	P	A	V	R	P	Q	P	W	V	P	S	L	F	S	C	T	L	P	L	I	L	L	S	L	W	
mGFra3	348	F	H	R	Q	L	F	S	Q	D	W	A	D	S	T	F	S	V	V	Q	Q	N	S	N	P	A	L	R	L	Q	P	R	L	P	I	L	S	F	S	I	L	P	L	I	L	Q	T	L	W		

FIG. 3

48613 1 MVRPLNPRPLPPVVLMLLLLLPPSPPLPLAAGDPLPTESRLMNSCLQARRK
48614 1 MVRPLNPRPLPPVVLMLLLLLPPSPPLPLAAGDPLPTESRLMNSCLQARRK

48613 51 CQADPTCSAAYYHHLDSCTSSISTPLPSEEPSVPADCLEAAQQLRNSSLIG
48614 51 CQADPTCSAAYYHHLDSCTSSISTPLPSEEPSVPADCLEAAQQLRNSSLIG

48613 101 CMCHRRMKNQVACLDIYWTVHRARSLGNYELDVSPYEDTVTSPWKMNLS
48614 101 CMCHRRMKNQVACLDIYWTVHRARSL.....

48613 151 KLNMLKP DSDLCLKFAMLCTLNDKCDRLRKAYGEACSGPHCQRHVCLRQL
48614 127 DSDLCLKFAMLCTLNDKCDRLRKAYGEACSGPHCQRHVCLRQL

48613 201 LTFEKA AEPAQGLLLCPCAPNDRGCGERRNTIAPNCALPPVAPNCLE
48614 170 LTFEKA AEPAQGLLLCPCAPNDRGCGERRNTIAPNCALPPVAPNCLE

48613 251 LRRLCFSDPLCRSRLVDFQTHCHPMDILGTCATEQSRCLRAYLGLIGTAM
48614 220 LRRLCFSDPLCRSRLVDFQTHCHPMDILGTCATEQSRCLRAYLGLIGTAM

48613 301 TPNFVSNVNTSVALSCTCRGSGNLQEECEMLEGFFSHNPCLTEAIAAKMR
48614 270 TPNFVSNVNTSVALSCTCRGSGNLQEECEMLEGFFSHNPCLTEAIAAKMR

48613 351 FHSQLFSQDWPHPHTFAVMAHQENPAVRPQPWPVPSLFSC TLPLILLSLW
48614 320 FHSQLFSQDWPHPHTFAVMAHQENPAVRPQPWPVPSLFSC TLPLILLSLW

FIG. 4

DNA48613.orf 1 A T G G T G C G C C C C C T G A C C C G C G A C C G C T G C C G C C C G T A G T C T G A T G T T
 GDNFRa1.orf 1 A T G A T C T T G G C A A C G T C T T C T G C C T C T T C T T C T
 GDNFRa2.orf 1 A T G A T C T T G G C A A C G T C T T C T G C C T C T T C T T C T T C T

DNA48613.orf 51 G C T G C T G C T G C C G C G T G C C G C T G C C T C T G C A G C C G A G A C C C C C
 GDNFRa1.orf 6 C C T G G C G A C C C T G T A C T T C G C G C T G C C G C T C T T G G A C T T G C T C C T G T C G G
 GDNFRa2.orf 39 A G A C G A G A C C C T C G C T C T T T G G C A G C C C T T C C C C T G C A G G C C C C G

DNA48613.orf 101 T T C C A C A G A A G C C G A C T C A T G A A C A G C T G T C T C C A G C C A G G A G A G
 GDNFRa1.orf 56 C C G A A G T G A G C G G C G A G A C C G C C T G G A T T G C G T G A A A G C C A G T G A T C A G
 GDNFRa2.orf 89 A G C T C A C A G G C T G G C G C C C C A G T G G A C T G T C C G G G C C A A T G A G C T G

DNA48613.orf 151 T G C C A G G C T G A T C C C A C C T G C A G T G C T G C T A C C A C C A C T G G A T T C C T G
 GDNFRa1.orf 106 T G C C T G A A G A G C A G A C T G C A G C A C A G T A C C G C A C G C T A A G G C A G T G
 GDNFRa2.orf 139 T G T G C C G C C G A T C C A A C T G C A G C T C T C G C T A C C G C A C T C T G C G G C A G T G

DNA48613.orf 201 C A C C T C T A G C A T A A G C A C C C A C T G C C C T . . . C A G A G A G C C T T C G G T C C
 GDNFRa1.orf 156 C G T G G C G G C A A G A G A C C A A C T T C A G C C T G G C A T C C G G C C T G G A G G C C A
 GDNFRa2.orf 189 C T G G C A G G C G C G A C C G C A C A C C A T G C T G G C C A

DNA48613.orf 248 C T G C T G A C T G C C T G G A G G C A G C A G C A A C T A G A C A G C T C T G A T A
 GDNFRa1.orf 206 A G A T G A G T G C C G C A G C G C C A T G G A G G C C C T G A A G C A G A A G T C G C T C T A C
 GDNFRa2.orf 224 A C A G A G A G T G C C A G G C G C C T T G G A G G T C T T G C A G G A G A G C C G C T G T A C

DNA48613.orf 298 G G C T G C A T G T G C C A C C G G C G C A T G A A G A A C A G G T T G C C T G C T T G G A C A T
 GDNFRa1.orf 256 A A C T G C C G C T G C A A G C G G G G T A T G A A G A A G G A G A A G A A C T G C C T G C G C A T
 GDNFRa2.orf 274 G A C T G C C G C T G C A A G C G G G G C A T G A A G A A G G A G C T G C A G T C T G C A G A T

DNA48613.orf 348 C T A T T G G A C C G T T C A C C G T G C C G C A G C C T T G G T A A C T A T G A G C T G G A T G
 GDNFRa1.orf 306 T T A C T G G A G C A T G T A C C A G A C C C T G C A G G G A A T G A T C T G C T G G A G G A T T
 GDNFRa2.orf 324 C T A C T G G A G C A T C C A C C T G G G G C T G A C C G A G G T G A G G A G T T C T A C G A A G

FIG. 5A

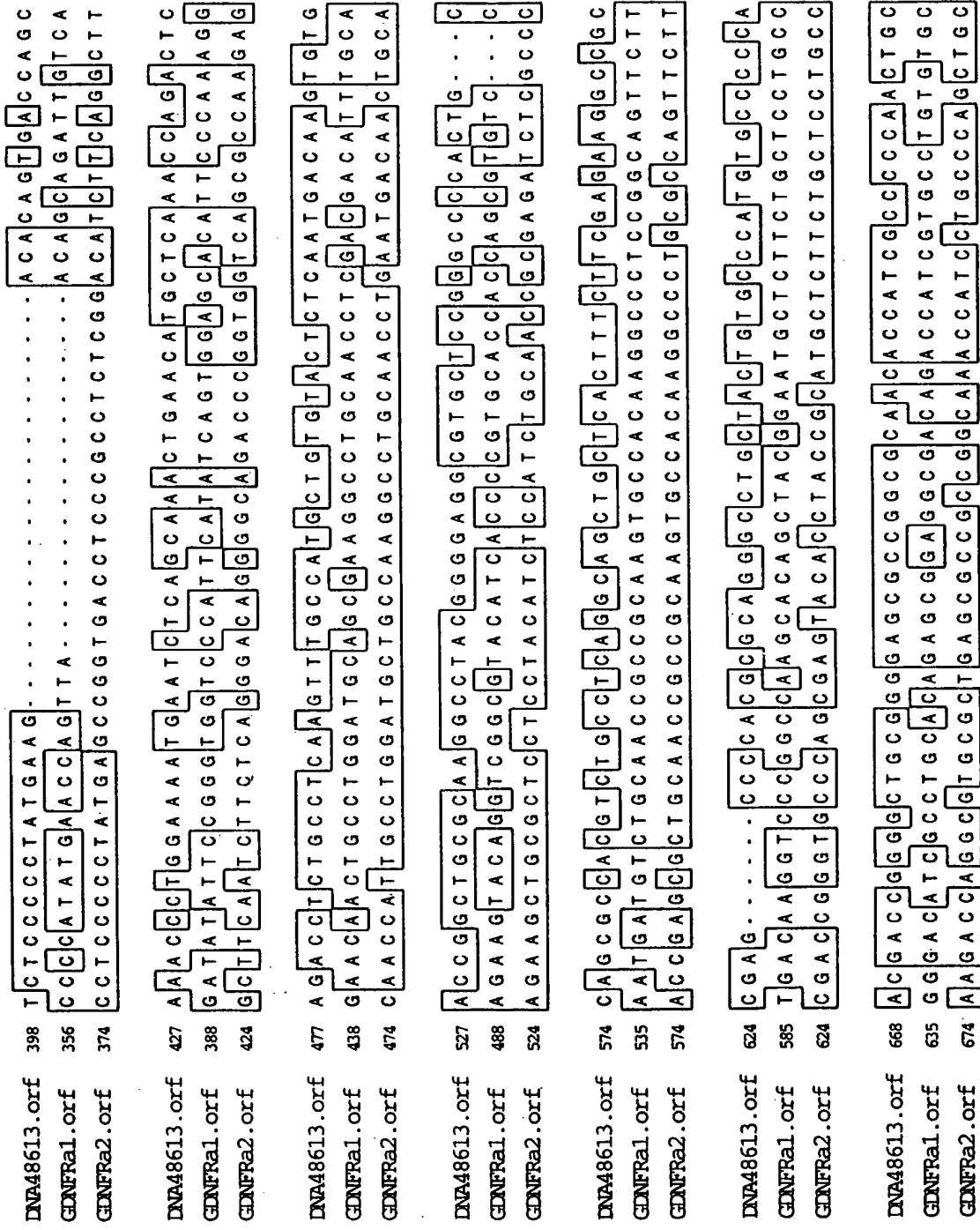


FIG. 5B

DNA48613.orf 1053 T C A C A G C C A A C T C T T C T C C C A G G A C T G G C C A C A C C C T A C C T T T G C T G T G A
 GENFRa1.orf 1029 C T C C G A T G T G A C C G T G T G G C A G C C A G C T T C C C A G T A C A G A C C A C C A C T G
 GENFRa2.orf 1074 C A C G G A C G T G A A C G T G T C C C C A A A G G C C C T C G T T C A G G C C A C C C A G G

 DNA48613.orf 1103 T G G C A C A C A G A A T G A A A C C C T G C T G T G A G G C C A C A G C C T G G G T G C C C
 GENFRa1.orf 1079 C C A C T A C C A C C A C T G C C C T C G G G T T A G A A C A A C C C T G G G C C A G C A
 GENFRa2.orf 1124 C C C C T C G G G T G G A G A A G A C G C C T T C T T T G C C A G A T G A C C T C A G T G A C A G T

 DNA48613.orf 1153 T C T C T T T C T C C T G C A C G C T T C C C T T G A T T C T G C T C C T G A G C C T A T G G T A
 GENFRa1.orf 1129 G G G T C T G A G A A T G A A A T T C C C A C T C A T G T T T T G C C A C C G T G T G C A A A T T T
 GENFRa2.orf 1174 A C A G C T T G G G A C C A G T G T C A T C A C C A C C T G C A C G T C T G T C C A G G A G C A

 DNA48613.orf 1203 G
 GENFRa1.orf 1179 A C A G G C A C A G A A G C T G A A A T C C A A T G T C G G G C A A T A C A C A C C T C T G T A
 GENFRa2.orf 1224 G G G C T G A A G G C C A A C A A C T C C A A A G A G T A A G C A T G T G C T T C A C A G A G C

 GENFRa1.orf 1229 T T T C A A T G G T A A T T A T G A A A A G A A G G T C T C G G T G C T T C C A G C C A C A T A
 GENFRa2.orf 1274 T C A C G A C A A A T A T C A T C C C A G G G A G T A A C A A G A G T A A G C A T G T G C T T C A C A G A G C

 GENFRa1.orf 1279 A C C A C A A A T C A A T G G C T G C T C C T C C A A G C T G T G G T C T G A G C C C A C T G C T
 GENFRa2.orf 1324 G G C C C C A G C A G A G C C A G A C C G T C G G C T G C C T T G A C C G T G C T G T C T G C T

 GENFRa1.orf 1329 G G T C C T G T G G T A A C C G C T C T G T C C A C C C T A T T A T C T T T A C A G A A A C A T
 GENFRa2.orf 1374 G A T G C T G A A C A G G C C T T G T A G

 GENFRa1.orf 1379 C A T A G

FIG. 5D

DNA48613 1 M V R P L N P R P L P P V L M L L L L P S P L P L A A G D P L P T E S R L M N S C L Q A R R K
GDNFrac1 1 M F L A T - - - L Y F A L - - P L L D L L L S A - - E V S G G D - - - - - R L - - D C V K A S D Q
GDNFrac2 1 M I L A N V F C L F F F L D E T L R S L A S P S - - S L Q G P E L H G W R P P V - - D C V R A N E L

DNA48613 51 C Q A D P T C S A A Y H H L D S C T S S I S T P L P - S E E P S V P A D C L E A A Q Q L R N S S L I
GDNFrac1 36 C L K E Q S C S T K Y R T L R Q C V A G K E T N F S L A S G L E A K D E C R S A M E A L K K K S L Y
GDNFrac2 47 C A A E S N C S S R Y R T L R Q C L A G R D R N - - - - - T M L A N K E C Q A A L E V L Q E S P L Y

DNA48613 100 G C M C H R R M K N Q V A C L D I Y W T V H R A R S L G N Y E L D V S P Y E D T V T S K P W K M N L
GDNFrac1 86 N C R C K R G M K K E K N C L R I Y W S M Y Q S L - Q G N D L L E D S P Y E P V N S R L S D I F R V
GDNFrac2 92 D C R C K R G M K K E L Q C L Q I Y W S I H L G L T E G E E F Y E A S P Y E P V T S R L S D I F R L

DNA48613 150 S K L - - - - - N M L K P D S D L C L K F A M L C T L N D K C D R L R K A Y G E A C S - - - - -
GDNFrac1 135 V P F I S - - - V E H I - - P K G N N C L D A A K A C N L D D I C K K Y R S A Y I T P C T T S V S -
GDNFrac2 142 A S I F S G T G A D P V V S A K S N H C L D A A K A C N L N D N C K K L R S S Y I S I C N R E I S P

DNA48613 188 G P H C Q R H V C L R O L L T F F E K A A E P H A Q G L L L C P C A P N D R G C G E R R R N T I A P
GDNFrac1 179 N D V C N R R K C H K A L R Q F F D K V P A K H S Y G M L F C S C - - R D I A C T E R R R Q T I V P
GDNFrac2 192 T E R C N R R K C H K A L R Q F F D R V P S E Y T Y R M L F C S C - - Q D Q A C A E R R R Q T I L P

DNA48613 238 N C A L P P V A - P N C L E L R R L C F S D P L C R S R L V D F Q T H C H P - M D I L G T C A T E Q
GDNFrac1 227 V C S Y E E R E K P N C L N L Q D S C K T N Y I C R S R L A D F F T N C Q P E S R S V S S C L K E N
GDNFrac2 240 S C S Y E D K E K P N C L D L R G V C R T D H L C R S R L A D F H A N C R A S Y Q T V T S C P A D N

DNA48613 286 - S R C L R A Y L G L I G T A M T P N F V S N V - - N T S V A L S C T C R G S G N L Q E E C E M L E
GDNFrac1 277 Y A D C L L A Y S G L I G T V M T P N Y I D S S - - S L S V A P W C D C S N S G N D L E E C L K F L
GDNFrac2 290 Y Q A C L G S Y A G M I G F D M T P N Y V D S S P T G I V V S P W C S C R G S G N M E E E C E K F L

DNA48613 333 G F F S H N P C L T E A I A A - - - - - K M R F H S Q L F S
GDNFrac1 325 N F F K D N T C L K N A I Q A F G N G S D V T V W Q P A F P V Q T T T A T T T T A L R V K N K P L G
GDNFrac2 340 R D F T E N P C L R N A I Q A F G N G T D V N V S P K G P S F Q A T Q A P R V E K T P S L P D D L S

DNA48613 358 Q - - - - - D W P H P T F A V M A H Q N E N P A V R P Q - - - - -
GDNFrac1 375 P A G S E N E I P T H V L P P C A N L Q A Q K L K S N V S G N T H L C I S N G N Y E K E G L G A S S
GDNFrac2 390 D S T S - - L G T S V I T T C T S V Q E Q G L K A N N S K E L S M C F T - - E L T T N I I P G S N

DNA48613 381 - - - - P W V P S L F S C T L P L I L L L S L W - - - - -
GDNFrac1 425 H I T T K S M A A P P S C G L S P L L V L V V T A L S T L L S L T E T S
GDNFrac2 435 K V I K P N S G P S R A R P S A A L T V L S V L M L K Q A L - - - - -

FIG. 6

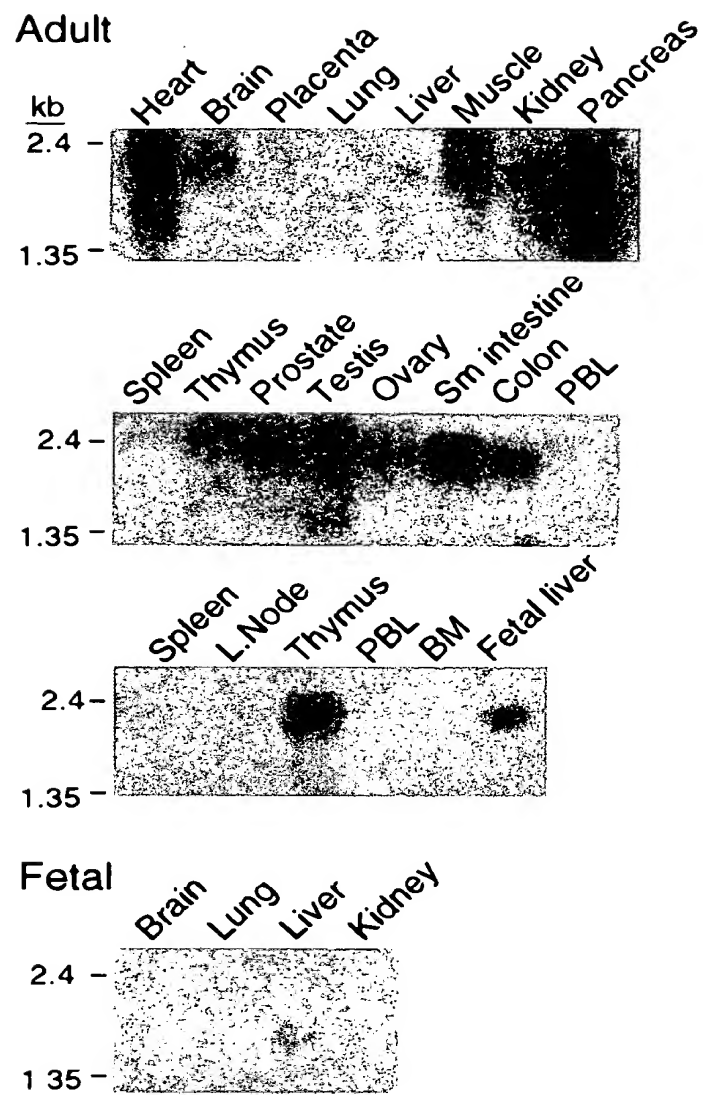


FIG. 7

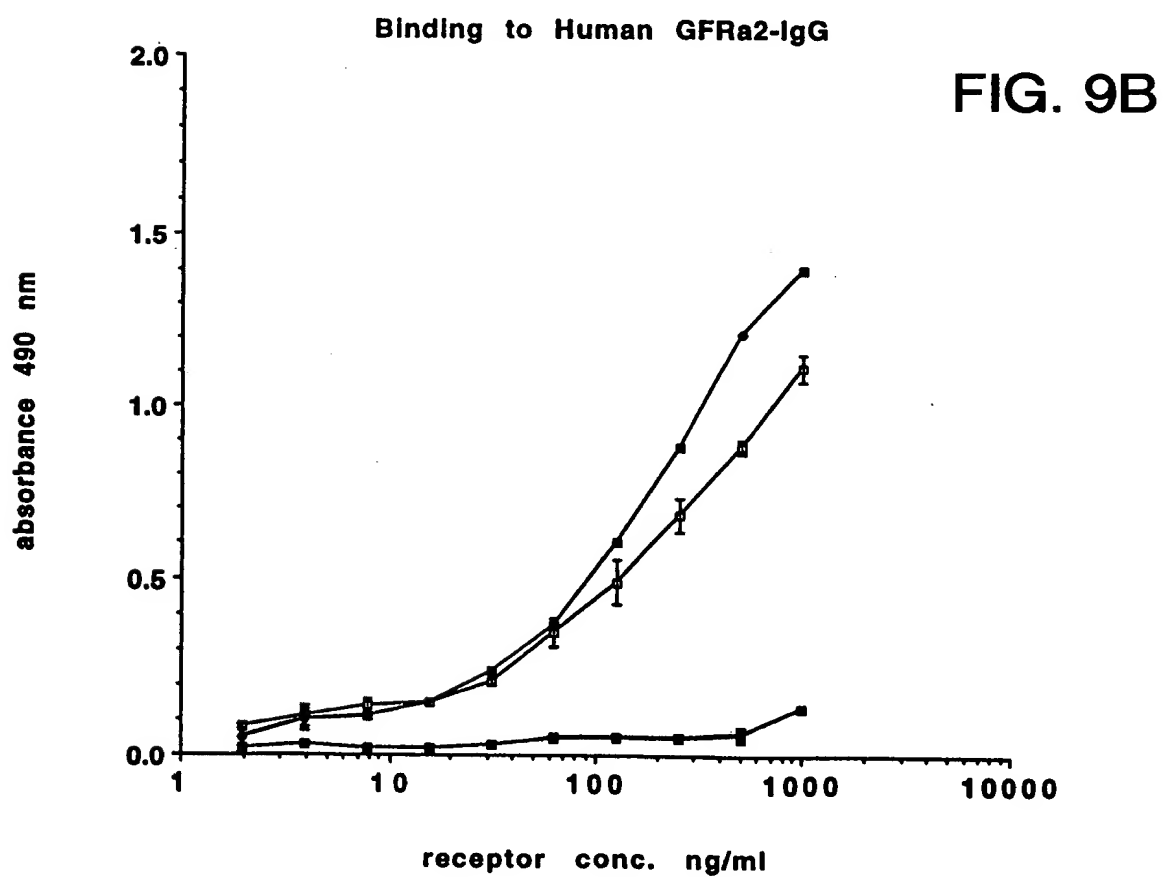
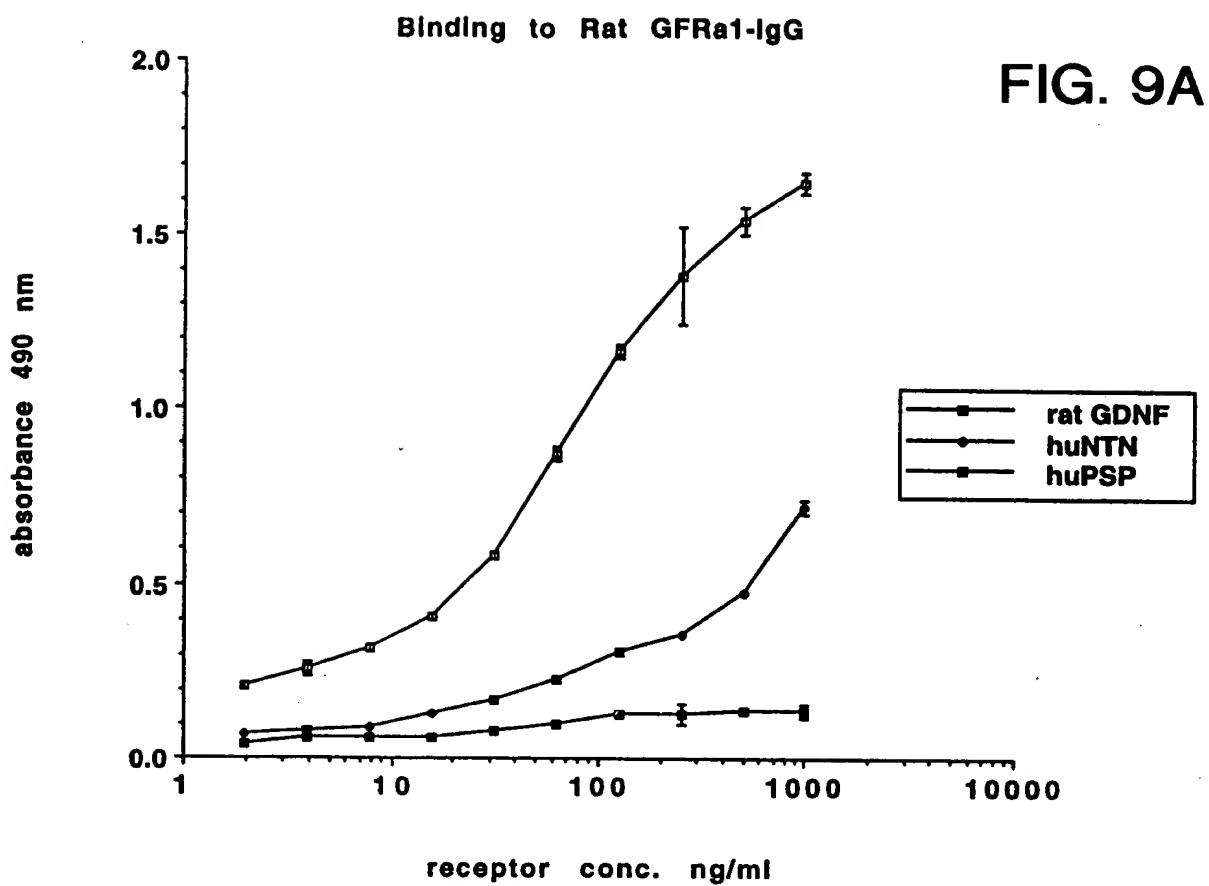
GFR α 1

GFR α 2

GFR α 3



FIG. 8



Binding to Human GFRa3-IgG

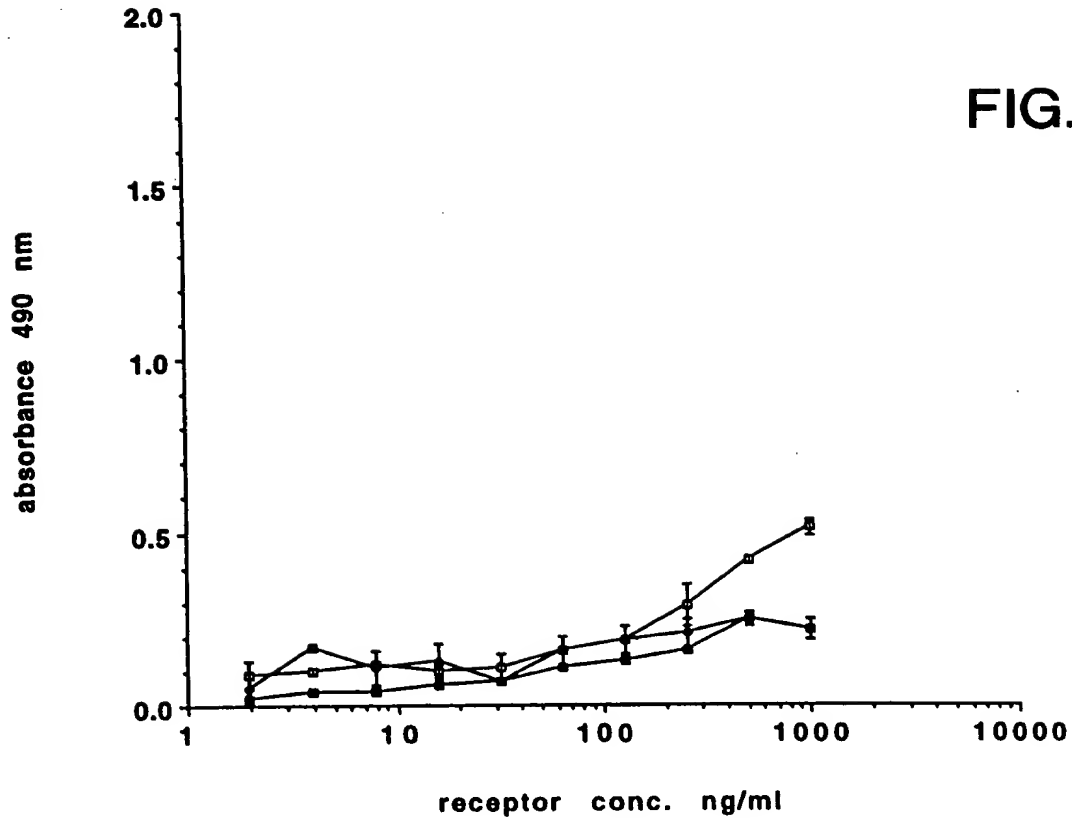


FIG. 9C

Proliferation of Ba/F3-GFRa2-mpl cells in response to NTN and GDNF

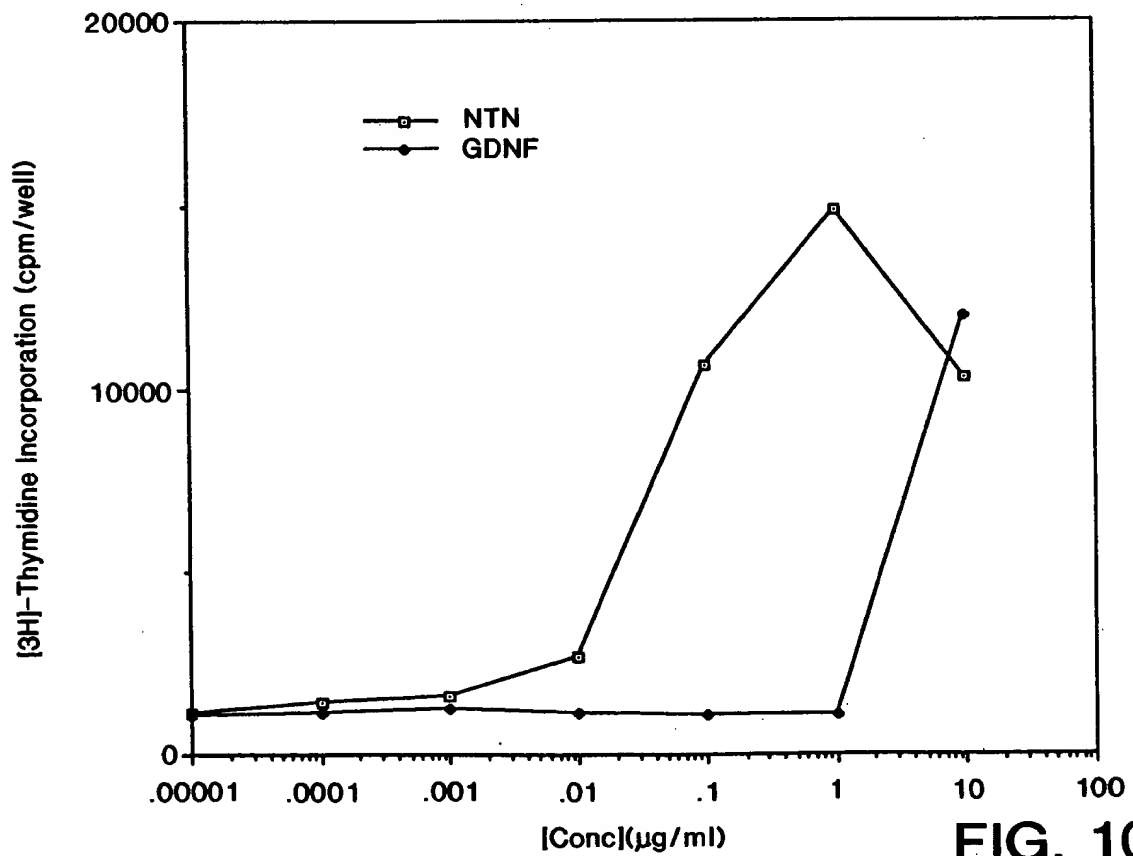


FIG. 10

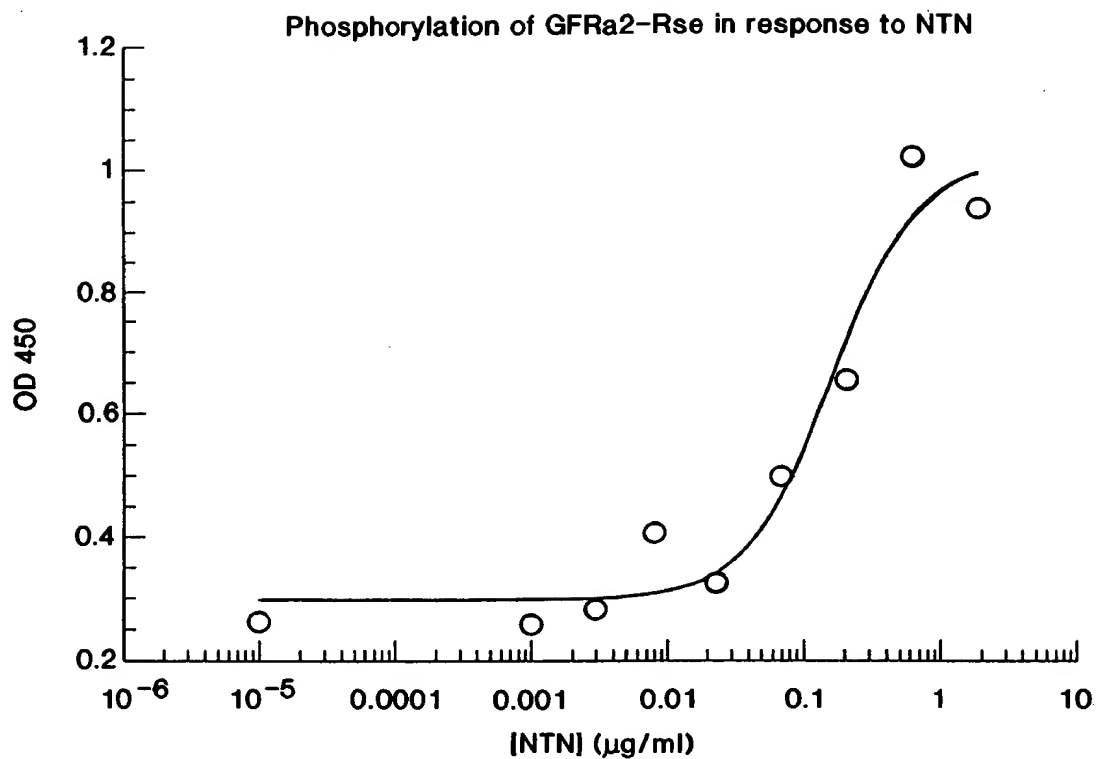


FIG. 11

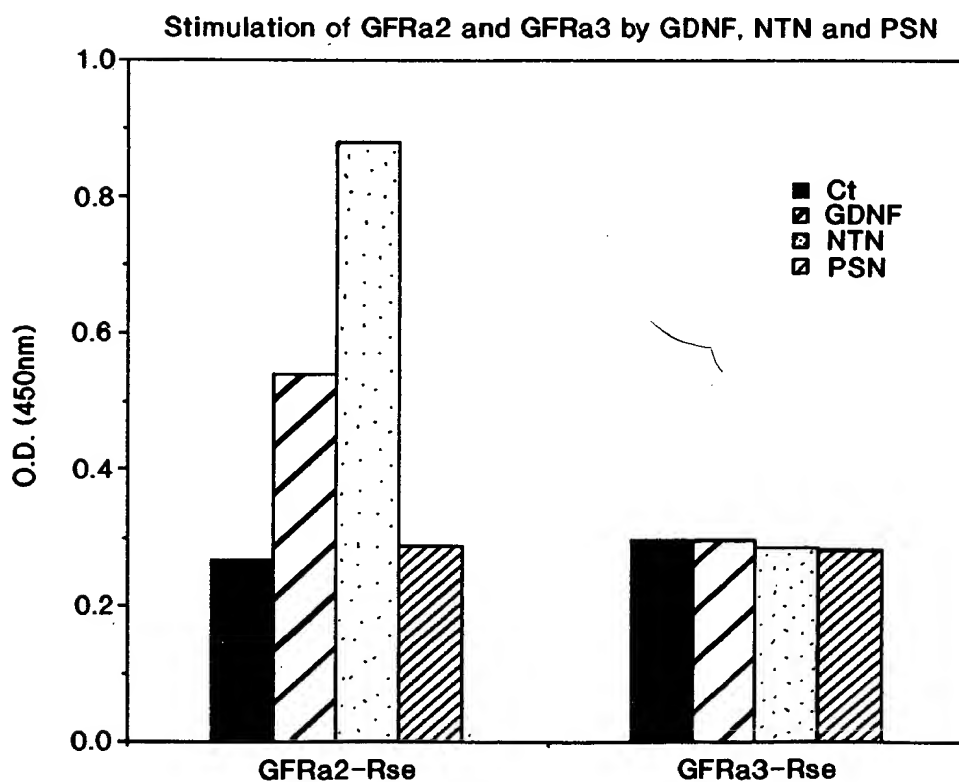


FIG. 12

Agonistic activity of anti gD mAbs in gD-alpha2-rse KIRA

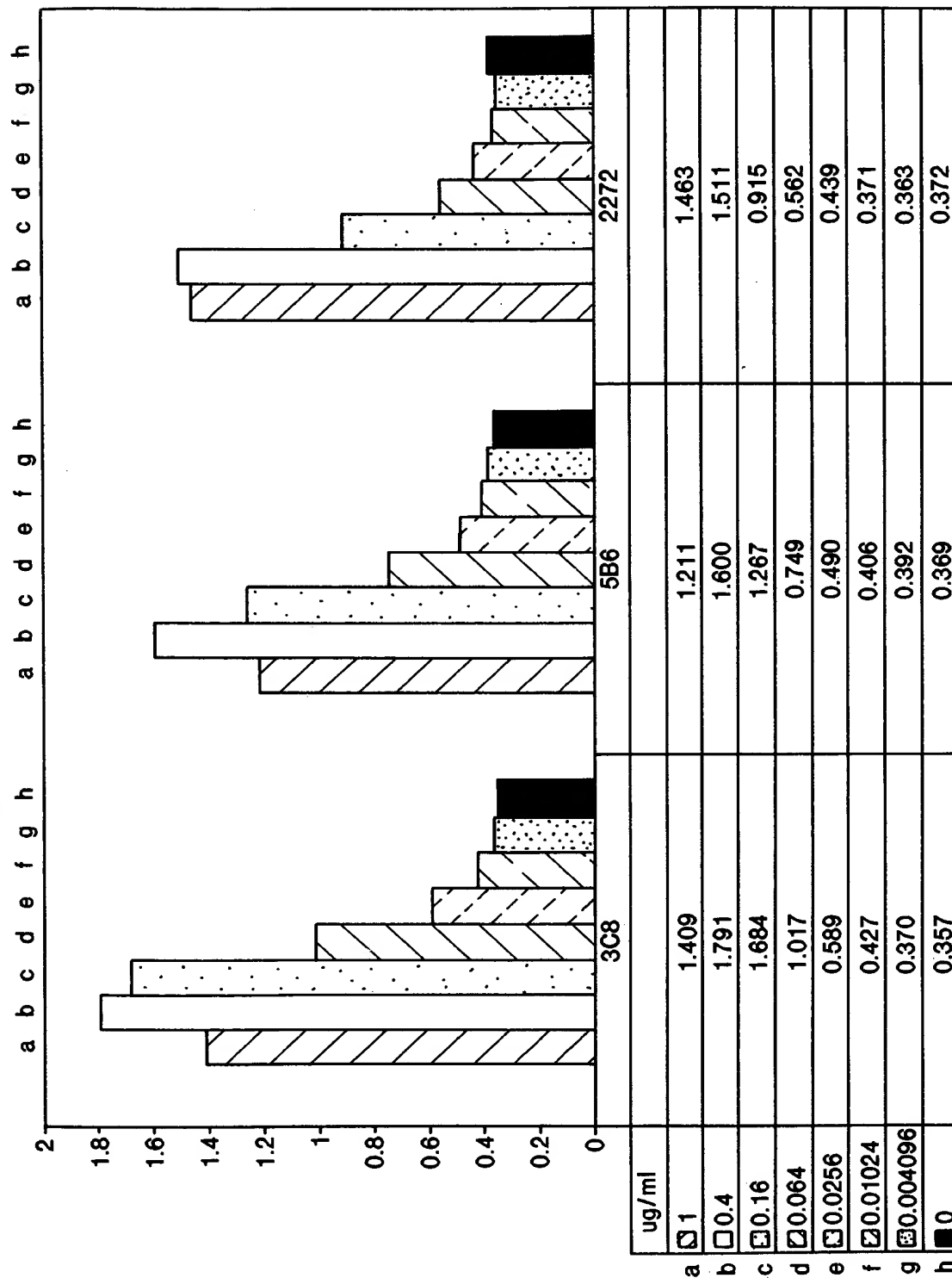


FIG. 13